

## SEQUENCE LISTING FREE TEXT

dgoA CDS for KDPGal Aldolase

dgoA CDS for KDPGal Aldolase

dgoA CDS for KDPGal Aldolase

aroB CDS for DHQ Synthase

tktA CDS for major Transketolase isozyme

tktB CDS for minor Transketolase isozyme

Primer JWF 430

Primer JWF 449

Primer JWF 484

Primer JWF 529

Primer JWF 501

Primer JWF 499

Primer JWF 541

Primer JWF 542

Primer JWF 610

Primer JWF 611

Primer JWF 625

Primer JWF 626

Primer JWF 541

Primer JWF 542

Primer JWF 636

Primer JWF 637

**Primer JWF 669**

**Primer JWF 670**

**Primer JWF 599**

**Primer JWF 560**

**Primer JWF 484**

**Primer JWF 529**

AP20R0301031417 22 MAR 2006

## SEQUENCE LISTING

<110> Board of Trustees operating Michigan State University  
Frost, John W.

<120> Methods and Materials for the Production of Shikimic Acid

<130> 6550-000086

<150> US 60/505,658

<151> 2003-09-24

<160> 34

<170> PatentIn version 3.3

<210> 1

<211> 618

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)..(615)

<223> dgoA CDS for KDPGal Aldolase

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Thr Pro Asp Glu Ala Leu Ala His Val Gly Ala Val Ile Asp Ala Gly	
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ttc gac gcg gtt gaa atc ccg ctg aat tcc cca caa tgg gag caa agc	144
Phe Asp Ala Val Glu Ile Pro Leu Asn Ser Pro Gln Trp Glu Gln Ser	
35 40 45	
att ccc gcc atc gtt gat gcg tac ggc gac aag gcg ttg att ggc gca	192
Ile Pro Ala Ile Val Asp Ala Tyr Gly Asp Lys Ala Leu Ile Gly Ala	
50 55 60	
ggt acg gta ctg aaa cct gaa cag gtc gat gcg ctc gcc agg atg ggc	240
Gly Thr Val Leu Lys Pro Glu Gln Val Asp Ala Leu Ala Arg Met Gly	
65 70 75 80	
tgt cag ctc atc gtt acg ccc aat atc cat agt gaa gtg atc cgc cgt	288
Cys Gln Leu Ile Val Thr Pro Asn Ile His Ser Glu Val Ile Arg Arg	
85 90 95	
gcg gtg ggc tac ggc atg acc gtc tgc ccc ggc tgc gcg acg gcg acc	336
Ala Val Gly Tyr Gly Met Thr Val Cys Pro Gly Cys Ala Thr Ala Thr	
100 105 110	

gaa gcc ttt acc gcg ctc gaa gcg ggc gcg cag gcg ctg aaa ata ttt 384  
 Glu Ala Phe Thr Ala Leu Glu Ala Gly Ala Gln Ala Leu Lys Ile Phe  
           115                                  120                                  125

ccg tca tcg gct ttt ggt ccg caa tac atc aaa gcg tta aaa gcg gta 432  
 Pro Ser Ser Ala Phe Gly Pro Gln Tyr Ile Lys Ala Leu Lys Ala Val  
           130                                  135                                  140

ttg cca tcg gac atc gca gtc ttt gcc gtt ggc ggc gtg acg cca gaa 480  
 Leu Pro Ser Asp Ile Ala Val Phe Ala Val Gly Gly Val Thr Pro Glu  
           145                                  150                                  155                                  160

aac ctg gcg cag tgg ata gac gca ggt tgt gca ggg gcg ggc tta ggc 528  
 Asn Leu Ala Gln Trp Ile Asp Ala Gly Cys Ala Gly Ala Gly Leu Gly  
                                   165                                  170                                  175

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 Ser Asp Leu Tyr Arg Ala Gly Gln Ser Val Glu Arg Thr Ala Gln Gln  
                                   180                                  185                                  190

gca gca gca ttt gtt aag gcg tat cga gag gca gtg caa tga 618  
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<213> Escherichia coli

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Phe Asp Ala Val Glu Ile Pro Leu Asn Ser Pro Gln Trp Glu Gln Ser  
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Gly Thr Val Leu Lys Pro Glu Gln Val Asp Ala Leu Ala Arg Met Gly  
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Cys Gln Leu Ile Val Thr Pro Asn Ile His Ser Glu Val Ile Arg Arg  
                                   85                                  90                                  95

Ala Val Gly Tyr Gly Met Thr Val Cys Pro Gly Cys Ala Thr Ala Thr  
100 105 110

Glu Ala Phe Thr Ala Leu Glu Ala Gly Ala Gln Ala Leu Lys Ile Phe  
115 120 125

Pro Ser Ser Ala Phe Gly Pro Gln Tyr Ile Lys Ala Leu Lys Ala Val  
130 135 140

Leu Pro Ser Asp Ile Ala Val Phe Ala Val Gly Gly Val Thr Pro Glu  
145 150 155 160

Asn Leu Ala Gln Trp Ile Asp Ala Gly Cys Ala Gly Ala Gly Leu Gly  
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Thr Pro Asp Glu Ala Leu Ala His Val Gly Ala Val Ile Asp Ala Gly  
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Phe Asp Ala Val Glu Ile Pro Leu Asn Ser Pro Gln Trp Glu Lys Ser  
35 40 45  
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Gly Thr Val Leu Gln Pro Glu Gln Val Asp Arg Leu Ala Ala Met Gly  
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 Cys Arg Leu Ile Val Thr Pro Asn Ile Gln Pro Glu Val Ile Arg Arg  
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 Ala Val Gly Tyr Gly Met Thr Val Cys Pro Gly Cys Ala Thr Ala Ser  
 100 105 110  
 gaa gcc ttt agc gcg ctc gat gcc ggc gcg cag gcg cta aaa atc ttc 384  
 Glu Ala Phe Ser Ala Leu Asp Ala Gly Ala Gln Ala Leu Lys Ile Phe  
 115 120 125  
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 Pro Ser Ser Ala Phe Gly Pro Asp Tyr Ile Lys Ala Leu Lys Ala Val  
 130 135 140  
 ctg ccg ccc gag gtt ccg gtc ttt gcc gtt ggc ggc gtg acg ccg gaa 480  
 Leu Pro Pro Glu Val Pro Val Phe Ala Val Gly Gly Val Thr Pro Glu  
 145 150 155 160  
 aac ctg gcg cag tgg att aat gcc ggc tgt gtt ggg gca gga ttg ggt 528  
 Asn Leu Ala Gln Trp Ile Asn Ala Gly Cys Val Gly Ala Gly Leu Gly  
 165 170 175  
 agc gat ctc tat cgt gcc ggc cag tcg gtt gaa cgt acc gcg cag cag 576  
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 gca gcc gca ttc gta aaa gcg tat cga gag gca gtg aaa tga 618  
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 Phe Asp Ala Val Glu Ile Pro Leu Asn Ser Pro Gln Trp Glu Lys Ser  
 35 40 45  
 Ile Pro Gln Val Val Asp Ala Tyr Gly Glu Gln Ala Leu Ile Gly Ala  
 50 55 60

Gly Thr Val Leu Gln Pro Glu Gln Val Asp Arg Leu Ala Ala Met Gly  
65 70 75 80

Cys Arg Leu Ile Val Thr Pro Asn Ile Gln Pro Glu Val Ile Arg Arg  
85 90 95

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100 105 110

Glu Ala Phe Ser Ala Leu Asp Ala Gly Ala Gln Ala Leu Lys Ile Phe  
115 120 125

Pro Ser Ser Ala Phe Gly Pro Asp Tyr Ile Lys Ala Leu Lys Ala Val  
130 135 140

Leu Pro Pro Glu Val Pro Val Phe Ala Val Gly Gly Val Thr Pro Glu  
145 150 155 160

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<223> dgoA CDS for KDPGal Aldolase

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1 5 10 15  
acg ccc gat gat gcc ctg gcg cac gtt ggc gcg gtg gtg gat gcg gga 96  
Thr Pro Asp Asp Ala Leu Ala His Val Gly Ala Val Val Asp Ala Gly  
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      35              40              45

a t t t c t t c c g t g g t g a a g g c g t a t g g c g g c a g g g c g c t t a t t g g c g c t      192
I l e S e r S e r V a l V a l L y s A l a T y r G l y G l y A r g A l a L e u I l e G l y A l a
      50              55              60

g g t a c c g t a c t g a a a c c g g a a c a g g t a g a c c a g c t t g c c g g g a t g g g c      240
G l y T h r V a l L e u L y s P r o G l u G l n V a l A s p G l n L e u A l a G l y M e t G l y
      65              70              75              80

t g c a a g c t g a t c g t c a c g c c g a a t a t c c a a c c g g a g g t g a t c c g c c g g      288
C y s L y s L e u I l e V a l T h r P r o A s n I l e G l n P r o G l u V a l I l e A r g A r g
      85              90              95

g c g g t g a g c t a t g g c a t g a c c g t g t g t c c g g g c t g c g c c a c g g c a a c g      336
A l a V a l S e r T y r G l y M e t T h r V a l C y s P r o G l y C y s A l a T h r A l a T h r
      100             105             110

g a a g c c t t t t c t g c g c t g g a t g c a g g c g c a c a g g c g t t a a a a t t t t c      384
G l u A l a P h e S e r A l a L e u A s p A l a G l y A l a G l n A l a L e u L y s I l e P h e
      115             120             125

c c g t c g t c g g c g t t g g t c c g g g c t a c a t c a g c g c g c t g a a a g c g g t a      432
P r o S e r S e r A l a P h e G l y P r o G l y T y r I l e S e r A l a L e u L y s A l a V a l
      130             135             140

c t t c c g c c g g a t g t t c c g c t a t t t g c c g t c g g c g g c g t g a c g c c g g a a      480
L e u P r o P r o A s p V a l P r o L e u P h e A l a V a l G l y G l y V a l T h r P r o G l u
      145             150             155             160

a a c c t a g c g c a a t g g a t t a a a g c a g g c t g t g t g g c g c g g g a t t g g g t      528
A s n L e u A l a G l n T r p I l e L y s A l a G l y C y s V a l G l y A l a G l y L e u G l y
      165             170             175

a g c g a t c t c t a t c g c g c c g g g c a a t c c g t t g a a c g c a c c g c g c a g c a g      576
S e r A s p L e u T y r A r g A l a G l y G l n S e r V a l G l u A r g T h r A l a G l n G l n
      180             185             190

g c t g c g g c a t t t g t t a a t g c g t a t c g a g a g g c a g t g a a a t g a      618
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35 40 45

Ile Ser Ser Val Val Lys Ala Tyr Gly Gly Arg Ala Leu Ile Gly Ala  
50 55 60

Gly Thr Val Leu Lys Pro Glu Gln Val Asp Gln Leu Ala Gly Met Gly  
65 70 75 80

Cys Lys Leu Ile Val Thr Pro Asn Ile Gln Pro Glu Val Ile Arg Arg  
85 90 95

Ala Val Ser Tyr Gly Met Thr Val Cys Pro Gly Cys Ala Thr Ala Thr  
100 105 110

Glu Ala Phe Ser Ala Leu Asp Ala Gly Ala Gln Ala Leu Lys Ile Phe  
115 120 125

Pro Ser Ser Ala Phe Gly Pro Gly Tyr Ile Ser Ala Leu Lys Ala Val  
130 135 140

Leu Pro Pro Asp Val Pro Leu Phe Ala Val Gly Gly Val Thr Pro Glu  
145 150 155 160

Asn Leu Ala Gln Trp Ile Lys Ala Gly Cys Val Gly Ala Gly Leu Gly  
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&lt;223&gt; aroB CDS for DHQ Synthase

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Ile Ala Ser Gly Leu Phe Asn Glu Pro Ala Ser Phe Leu Pro Leu Lys	
20 25 30	
tcg ggc gag cag gtc atg ttg gtc acc aac gaa acc ctg gct cct ctg	144
Ser Gly Glu Gln Val Met Leu Val Thr Asn Glu Thr Leu Ala Pro Leu	
35 40 45	
tat ctc gat aag gtc cgc ggc gta ctt gaa cag gcg ggt gtt aac gtc	192
Tyr Leu Asp Lys Val Arg Gly Val Leu Glu Gln Ala Gly Val Asn Val	
50 55 60	
gat agc gtt atc ctc cct gac ggc gag cag tat aaa agc ctg gct gta	240
Asp Ser Val Ile Leu Pro Asp Gly Glu Gln Tyr Lys Ser Leu Ala Val	
65 70 75 80	
ctc gat acc gtc ttt acg gcg ttg tta caa aaa ccg cat ggt cgc gat	288
Leu Asp Thr Val Phe Thr Ala Leu Leu Gln Lys Pro His Gly Arg Asp	
85 90 95	
act acg ctg gtg gcg ctt ggc ggc ggc gta gtg ggc gat ctg acc ggc	336
Thr Thr Leu Val Ala Leu Gly Gly Gly Val Val Gly Asp Leu Thr Gly	
100 105 110	
ttc gcg gcg gcg agt tat cag cgc ggt gtc cgt ttc att caa gtc ccg	384
Phe Ala Ala Ser Tyr Gln Arg Gly Val Arg Phe Ile Gln Val Pro	
115 120 125	
acg acg tta ctg tcg cag gtc gat tcc tcc gtt ggc ggc aaa act gcg	432
Thr Thr Leu Leu Ser Gln Val Asp Ser Ser Val Gly Gly Lys Thr Ala	
130 135 140	
gtc aac cat ccc ctc ggt aaa aac atg att ggc gcg ttc tac caa cct	480
Val Asn His Pro Leu Gly Lys Asn Met Ile Gly Ala Phe Tyr Gln Pro	
145 150 155 160	
gct tca gtg gtg gtg gat ctc gac tgt ctg aaa acg ctt ccc ccg cgt	528
Ala Ser Val Val Val Asp Leu Asp Cys Leu Lys Thr Leu Pro Pro Arg	
165 170 175	
gag tta gcg tcg ggg ctg gca gaa gtc atc aaa tac ggc att att ctt	576
Glu Leu Ala Ser Gly Leu Ala Glu Val Ile Lys Tyr Gly Ile Ile Leu	
180 185 190	
gac ggt gcg ttt ttt aac tgg ctg gaa gag aat ctg gat gcg ttg ttg	624
Asp Gly Ala Phe Phe Asn Trp Leu Glu Glu Asn Leu Asp Ala Leu Leu	
195 200 205	
cgt ctg gac ggt ccg gca atg gcg tac tgt att cgc cgt tgt tgt gaa	672

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225                               230                               235                               240

gct tta ctg aat ctg gga cac acc ttt ggt cat gcc att gaa gct gaa      768
Ala Leu Leu Asn Leu Gly His Thr Phe Gly His Ala Ile Glu Ala Glu
245                               250                               255

atg ggg tat ggc aat tgg tta cat ggt gaa gcg gtc gct gcg ggt atg      816
Met Gly Tyr Gly Asn Trp Leu His Gly Glu Ala Val Ala Ala Gly Met
260                               265                               270

gtg atg gcg gcg cgg acg tcg gaa cgt ctc ggg cag ttt agt tct gcc      864
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275                               280                               285

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Glu Thr Gln Arg Ile Ile Thr Leu Leu Lys Arg Ala Gly Leu Pro Val
290                               295                               300

aat ggg ccg cgc gaa atg tcc gcg cag gcg tat tta ccg cat atg ctg      960
Asn Gly Pro Arg Glu Met Ser Ala Gln Ala Tyr Leu Pro His Met Leu
305                               310                               315                               320

cgt gac aag aaa gtc ctt gcg gga gag atg cgc tta att ctt ccg ttg      1008
Arg Asp Lys Lys Val Leu Ala Gly Glu Met Arg Leu Ile Leu Pro Leu
325                               330                               335

gca att ggt aag agt gaa gtt cgc agc ggc gtt tcg cac gag ctt gtt      1056
Ala Ile Gly Lys Ser Glu Val Arg Ser Gly Val Ser His Glu Leu Val
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Asp Ser Val Ile Leu Pro Asp Gly Glu Gln Tyr Lys Ser Leu Ala Val  
 65 70 75 80

Leu Asp Thr Val Phe Thr Ala Leu Leu Gln Lys Pro His Gly Arg Asp  
 85 90 95

Thr Thr Leu Val Ala Leu Gly Gly Gly Val Val Gly Asp Leu Thr Gly  
 100 105 110

Phe Ala Ala Ala Ser Tyr Gln Arg Gly Val Arg Phe Ile Gln Val Pro  
 115 120 125

Thr Thr Leu Leu Ser Gln Val Asp Ser Ser Val Gly Gly Lys Thr Ala  
 130 135 140

Val Asn His Pro Leu Gly Lys Asn Met Ile Gly Ala Phe Tyr Gln Pro  
 145 150 155 160

Ala Ser Val Val Val Asp Leu Asp Cys Leu Lys Thr Leu Pro Pro Arg  
 165 170 175

Glu Leu Ala Ser Gly Leu Ala Glu Val Ile Lys Tyr Gly Ile Ile Leu  
 180 185 190

Asp Gly Ala Phe Phe Asn Trp Leu Glu Glu Asn Leu Asp Ala Leu Leu  
 195 200 205

Arg Leu Asp Gly Pro Ala Met Ala Tyr Cys Ile Arg Arg Cys Cys Glu  
 210 215 220

Leu Lys Ala Glu Val Val Ala Ala Asp Glu Arg Glu Thr Gly Leu Arg  
 225 230 235 240

Ala Leu Leu Asn Leu Gly His Thr Phe Gly His Ala Ile Glu Ala Glu  
 245 250 255

Met Gly Tyr Gly Asn Trp Leu His Gly Glu Ala Val Ala Ala Gly Met  
 260 265 270

Val Met Ala Ala Arg Thr Ser Glu Arg Leu Gly Gln Phe Ser Ser Ala  
275 280 285

Glu Thr Gln Arg Ile Ile Thr Leu Leu Lys Arg Ala Gly Leu Pro Val  
290 295 300

Asn Gly Pro Arg Glu Met Ser Ala Gln Ala Tyr Leu Pro His Met Leu  
305 310 315 320

Arg Asp Lys Lys Val Leu Ala Gly Glu Met Arg Leu Ile Leu Pro Leu  
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<223> tktA CDS for major Tranketolase isozyme

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gac gca gta cag aaa gcc aaa tcc ggt cac ccg ggt gcc cct atg ggt 96  
Asp Ala Val Gln Lys Ala Lys Ser Gly His Pro Gly Ala Pro Met Gly  
20 25 30  
atg gct gac att gcc gaa gtc ctg tgg cgt gat ttc ctg aaa cac aac 144  
Met Ala Asp Ile Ala Glu Val Leu Trp Arg Asp Phe Leu Lys His Asn  
35 40 45  
ccg cag aat ccg tcc tgg gct gac cgt gac cgc ttc gtg ctg tcc aac 192  
Pro Gln Asn Pro Ser Trp Ala Asp Arg Asp Arg Phe Val Leu Ser Asn  
50 55 60  
ggc cac ggc tcc atg ctg atc tac agc ctg ctg cac ctc acc ggt tac 240  
Gly His Gly Ser Met Leu Ile Tyr Ser Leu Leu His Leu Thr Gly Tyr  
65 70 75 80

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Asp Leu Pro Met Glu Glu Leu Lys Asn Phe Arg Gln Leu His Ser Lys	
85 90 95	
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Thr Pro Gly His Pro Glu Val Gly Tyr Thr Ala Gly Val Glu Thr Thr	
100 105 110	
acc ggt ccg ctg ggt cag ggt att gcc aac gca gtc ggt atg gcg att	384
Thr Gly Pro Leu Gly Gln Gly Ile Ala Asn Ala Val Gly Met Ala Ile	
115 120 125	
gca gaa aaa acg ctg gcg gcg cag ttt aac cgt ccg ggc cac gac att	432
Ala Glu Lys Thr Leu Ala Ala Gln Phe Asn Arg Pro Gly His Asp Ile	
130 135 140	
gtc gac cac tac acc tac gcc ttc atg ggc gac ggc tgc atg atg gaa	480
Val Asp His Tyr Thr Tyr Ala Phe Met Gly Asp Gly Cys Met Met Glu	
145 150 155 160	
ggc atc tcc cac gaa gtt tgc tct ctg gcg ggt acg ctg aag ctg ggt	528
Gly Ile Ser His Glu Val Cys Ser Leu Ala Gly Thr Leu Lys Leu Gly	
165 170 175	
aaa ctg att gca ttc tac gat gac aac ggt att tct atc gat ggt cac	576
Lys Leu Ile Ala Phe Tyr Asp Asp Asn Gly Ile Ser Ile Asp Gly His	
180 185 190	
gtt gaa ggc tgg ttc acc gac gac acc gca atg cgt ttc gaa gct tac	624
Val Glu Gly Trp Phe Thr Asp Asp Thr Ala Met Arg Phe Glu Ala Tyr	
195 200 205	
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Gly Trp His Val Ile Arg Asp Ile Asp Gly His Asp Ala Ala Ser Ile	
210 215 220	
aaa cgc gca gta gaa gaa gcg cgc gca gtg act gac aaa cct tcc ctg	720
Lys Arg Ala Val Glu Glu Ala Arg Ala Val Thr Asp Lys Pro Ser Leu	
225 230 235 240	
ctg atg tgc aaa acc atc atc ggt ttc ggt tcc ccg aac aaa gcc ggt	768
Leu Met Cys Lys Thr Ile Ile Gly Phe Gly Ser Pro Asn Lys Ala Gly	
245 250 255	
acc cac gac tcc cac ggt gcg ccg ctg ggc gac gct gaa att gcc ctg	816
Thr His Asp Ser His Gly Ala Pro Leu Gly Asp Ala Glu Ile Ala Leu	
260 265 270	
acc cgc gaa caa ctg ggc tgg aaa tat gcg ccg ttc gaa atc ccg tct	864
Thr Arg Glu Gln Leu Gly Trp Lys Tyr Ala Pro Phe Glu Ile Pro Ser	
275 280 285	
gaa atc tat gct cag tgg gat gcg aaa gaa gca ggc cag gcg aaa gaa	912
Glu Ile Tyr Ala Gln Trp Asp Ala Lys Glu Ala Gly Gln Ala Lys Glu	
290 295 300	
tcc gca tgg aac gag aaa ttc gct gct tac gcg aaa gct tat ccg cag	960

Ser	Ala	Trp	Asn	Glu	Lys	Phe	Ala	Ala	Tyr	Ala	Lys	Ala	Tyr	Pro	Gln	
305					310					315					320	
gaa gcc gct gaa ttt acc cgc cgt atg aaa ggc gaa atg ccg tct gac																1008
Glu	Ala	Ala	Glu	Phe	Thr	Arg	Arg	Met	Lys	Gly	Glu	Met	Pro	Ser	Asp	
				325					330					335		
ttc gac gct aaa gcg aaa gag ttc atc gct aaa ctg cag gct aat ccg																1056
Phe	Asp	Ala	Lys	Ala	Lys	Glu	Phe	Ile	Ala	Lys	Leu	Gln	Ala	Asn	Pro	
			340					345					350			
gcg aaa atc gcc agc cgt aaa gcg tct cag aat gct atc gaa gcg ttc																1104
Ala	Lys	Ile	Ala	Ser	Arg	Lys	Ala	Ser	Gln	Asn	Ala	Ile	Glu	Ala	Phe	
		355					360					365				
ggg ccg ctg ttg ccg gaa ttc ctc ggc ggt tct gct gac ctg gcg ccg																1152
Gly	Pro	Leu	Leu	Pro	Glu	Phe	Leu	Gly	Gly	Ser	Ala	Asp	Leu	Ala	Pro	
	370					375					380					
tct aac ctg acc ctg tgg tct ggt tct aaa gca atc aac gaa gat gct																1200
Ser	Asn	Leu	Thr	Leu	Trp	Ser	Gly	Ser	Lys	Ala	Ile	Asn	Glu	Asp	Ala	
385					390					395					400	
gcg ggt aac tac atc cac tac ggt gtt cgc gag ttc ggt atg acc gcg																1248
Ala	Gly	Asn	Tyr	Ile	His	Tyr	Gly	Val	Arg	Glu	Phe	Gly	Met	Thr	Ala	
			405					410					415			
att gct aac ggt atc tcc ctg cac ggt ggc ttc ctg ccg tac acc tcc																1296
Ile	Ala	Asn	Gly	Ile	Ser	Leu	His	Gly	Gly	Phe	Leu	Pro	Tyr	Thr	Ser	
			420					425					430			
acc ttc ctg atg ttc gtg gaa tac gca cgt aac gcc gta cgt atg gct																1344
Thr	Phe	Leu	Met	Phe	Val	Glu	Tyr	Ala	Arg	Asn	Ala	Val	Arg	Met	Ala	
		435					440					445				
gcg ctg atg aaa cag cgt cag gtg atg gtt tac acc cac gac tcc atc																1392
Ala	Leu	Met	Lys	Gln	Arg	Gln	Val	Met	Val	Tyr	Thr	His	Asp	Ser	Ile	
	450					455					460					
ggg ctg ggc gaa gac ggg ccg act cac cag ccg gtt gag cag gtc gct																1440
Gly	Leu	Gly	Glu	Asp	Gly	Pro	Thr	His	Gln	Pro	Val	Glu	Gln	Val	Ala	
465					470					475					480	
tct ctg cgc gta acc ccg aac atg tct aca tgg cgt ccg tgt gac cag																1488
Ser	Leu	Arg	Val	Thr	Pro	Asn	Met	Ser	Thr	Trp	Arg	Pro	Cys	Asp	Gln	
				485					490					495		
gtt gaa tcc gcg gtc gcg tgg aaa tac ggt gtt gag cgt cag gac ggc																1536
Val	Glu	Ser	Ala	Val	Ala	Trp	Lys	Tyr	Gly	Val	Glu	Arg	Gln	Asp	Gly	
			500					505					510			
ccg acc gca ctg atc ctc tcc cgt cag aac ctg gcg cag cag gaa cga																1584
Pro	Thr	Ala	Leu	Ile	Leu	Ser	Arg	Gln	Asn	Leu	Ala	Gln	Gln	Glu	Arg	
		515					520					525				
act gaa gag caa ctg gca aac atc gcg cgc ggt ggt tat gtg ctg aaa																1632
Thr	Glu	Glu	Gln	Leu	Ala	Asn	Ile	Ala	Arg	Gly	Gly	Tyr	Val	Leu	Lys	

530	535	540	
gac tgc gcc ggt cag ccg gaa ctg att ttc atc gct acc ggt tca gaa			1680
Asp Cys Ala Gly Gln Pro Glu Leu Ile Phe Ile Ala Thr Gly Ser Glu			
545	550	555	560
ggt gaa ctg gct gtt gct gcc tac gaa aaa ctg act gcc gaa ggc gtg			1728
Val Glu Leu Ala Val Ala Ala Tyr Glu Lys Leu Thr Ala Glu Gly Val			
	565	570	575
aaa gcg cgc gtg gtg tcc atg tcg tct acc gac gca ttt gac aag cag			1776
Lys Ala Arg Val Ser Met Ser Ser Thr Asp Ala Phe Asp Lys Gln			
	580	585	590
gat gct gct tac cgt gaa tcc gta ctg ccg aaa gcg gtt act gca cgc			1824
Asp Ala Ala Tyr Arg Glu Ser Val Leu Pro Lys Ala Val Thr Ala Arg			
	595	600	605
gtt gct gta gaa gcg ggt att gct gac tac tgg tac aag tat gtt ggc			1872
Val Ala Val Glu Ala Gly Ile Ala Asp Tyr Trp Tyr Lys Tyr Val Gly			
	610	615	620
ctg aac ggt gct atc gtc ggt atg acc acc ttc ggt gaa tct gct ccg			1920
Leu Asn Gly Ala Ile Val Gly Met Thr Thr Phe Gly Glu Ser Ala Pro			
	625	630	635
gca gag ctg ctg ttt gaa gag ttc ggc ttc act gtt gat aac gtt gtt			1968
Ala Glu Leu Leu Phe Glu Glu Phe Gly Phe Thr Val Asp Asn Val Val			
	645	650	655
gcg aaa gca aaa gaa ctg ctg taa			1992
Ala Lys Ala Lys Glu Leu Leu			
	660		

&lt;210&gt; 10

&lt;211&gt; 663

&lt;212&gt; PRT

&lt;213&gt; Escherichia coli

&lt;400&gt; 10

Met Ser Ser Arg Lys Glu Leu Ala Asn Ala Ile Arg Ala Leu Ser Met
1 5 10 15

Asp Ala Val Gln Lys Ala Lys Ser Gly His Pro Gly Ala Pro Met Gly
20 25 30

Met Ala Asp Ile Ala Glu Val Leu Trp Arg Asp Phe Leu Lys His Asn
35 40 45

Pro Gln Asn Pro Ser Trp Ala Asp Arg Asp Arg Phe Val Leu Ser Asn
50 55 60



Gly His Gly Ser Met Leu Ile Tyr Ser Leu Leu His Leu Thr Gly Tyr  
65 70 75 80

Asp Leu Pro Met Glu Glu Leu Lys Asn Phe Arg Gln Leu His Ser Lys  
85 90 95

Thr Pro Gly His Pro Glu Val Gly Tyr Thr Ala Gly Val Glu Thr Thr  
100 105 110

Thr Gly Pro Leu Gly Gln Gly Ile Ala Asn Ala Val Gly Met Ala Ile  
115 120 125

Ala Glu Lys Thr Leu Ala Ala Gln Phe Asn Arg Pro Gly His Asp Ile  
130 135 140

Val Asp His Tyr Thr Tyr Ala Phe Met Gly Asp Gly Cys Met Met Glu  
145 150 155 160

Gly Ile Ser His Glu Val Cys Ser Leu Ala Gly Thr Leu Lys Leu Gly  
165 170 175

Lys Leu Ile Ala Phe Tyr Asp Asp Asn Gly Ile Ser Ile Asp Gly His  
180 185 190

Val Glu Gly Trp Phe Thr Asp Asp Thr Ala Met Arg Phe Glu Ala Tyr  
195 200 205

Gly Trp His Val Ile Arg Asp Ile Asp Gly His Asp Ala Ala Ser Ile  
210 215 220

Lys Arg Ala Val Glu Glu Ala Arg Ala Val Thr Asp Lys Pro Ser Leu  
225 230 235 240

Leu Met Cys Lys Thr Ile Ile Gly Phe Gly Ser Pro Asn Lys Ala Gly  
245 250 255

Thr His Asp Ser His Gly Ala Pro Leu Gly Asp Ala Glu Ile Ala Leu  
260 265 270

Thr Arg Glu Gln Leu Gly Trp Lys Tyr Ala Pro Phe Glu Ile Pro Ser  
275 280 285

Glu Ile Tyr Ala Gln Trp Asp Ala Lys Glu Ala Gly Gln Ala Lys Glu  
 290 295 300  
 Ser Ala Trp Asn Glu Lys Phe Ala Ala Tyr Ala Lys Ala Tyr Pro Gln  
 305 310 315 320  
 Glu Ala Ala Glu Phe Thr Arg Arg Met Lys Gly Glu Met Pro Ser Asp  
 325 330 335  
 Phe Asp Ala Lys Ala Lys Glu Phe Ile Ala Lys Leu Gln Ala Asn Pro  
 340 345 350  
 Ala Lys Ile Ala Ser Arg Lys Ala Ser Gln Asn Ala Ile Glu Ala Phe  
 355 360 365  
 Gly Pro Leu Leu Pro Glu Phe Leu Gly Gly Ser Ala Asp Leu Ala Pro  
 370 375 380  
 Ser Asn Leu Thr Leu Trp Ser Gly Ser Lys Ala Ile Asn Glu Asp Ala  
 385 390 395 400  
 Ala Gly Asn Tyr Ile His Tyr Gly Val Arg Glu Phe Gly Met Thr Ala  
 405 410 415  
 Ile Ala Asn Gly Ile Ser Leu His Gly Gly Phe Leu Pro Tyr Thr Ser  
 420 425 430  
 Thr Phe Leu Met Phe Val Glu Tyr Ala Arg Asn Ala Val Arg Met Ala  
 435 440 445  
 Ala Leu Met Lys Gln Arg Gln Val Met Val Tyr Thr His Asp Ser Ile  
 450 455 460  
 Gly Leu Gly Glu Asp Gly Pro Thr His Gln Pro Val Glu Gln Val Ala  
 465 470 475 480  
 Ser Leu Arg Val Thr Pro Asn Met Ser Thr Trp Arg Pro Cys Asp Gln  
 485 490 495  
 Val Glu Ser Ala Val Ala Trp Lys Tyr Gly Val Glu Arg Gln Asp Gly  
 500 505 510  
 Pro Thr Ala Leu Ile Leu Ser Arg Gln Asn Leu Ala Gln Gln Glu Arg

515

520

525

Thr Glu Glu Gln Leu Ala Asn Ile Ala Arg Gly Gly Tyr Val Leu Lys  
 530 535 540

Asp Cys Ala Gly Gln Pro Glu Leu Ile Phe Ile Ala Thr Gly Ser Glu  
 545 550 555 560

Val Glu Leu Ala Val Ala Ala Tyr Glu Lys Leu Thr Ala Glu Gly Val  
 565 570 575

Lys Ala Arg Val Val Ser Met Ser Ser Thr Asp Ala Phe Asp Lys Gln  
 580 585 590

Asp Ala Ala Tyr Arg Glu Ser Val Leu Pro Lys Ala Val Thr Ala Arg  
 595 600 605

Val Ala Val Glu Ala Gly Ile Ala Asp Tyr Trp Tyr Lys Tyr Val Gly  
 610 615 620

Leu Asn Gly Ala Ile Val Gly Met Thr Thr Phe Gly Glu Ser Ala Pro  
 625 630 635 640

Ala Glu Leu Leu Phe Glu Glu Phe Gly Phe Thr Val Asp Asn Val Val  
 645 650 655

Ala Lys Ala Lys Glu Leu Leu  
 660

&lt;210&gt; 11

&lt;211&gt; 2004

&lt;212&gt; DNA

&lt;213&gt; Escherichia coli

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(2001)

&lt;223&gt; tktB CDS for minor Transketolase isozyme

&lt;400&gt; 11

atg tcc cga aaa gac ctt gcc aat gcg att cgc gca ctc agt atg gat 48  
 Met Ser Arg Lys Asp Leu Ala Asn Ala Ile Arg Ala Leu Ser Met Asp  
 1 5 10 15

gcg gta caa aaa gcc aac tct ggt cat ccc ggc gcg ccg atg ggc atg 96  
 Ala Val Gln Lys Ala Asn Ser Gly His Pro Gly Ala Pro Met Gly Met

20	25	30	
gct gat att gcc gaa gtg ctg tgg aac gat ttt ctt aaa cat aac cct Ala Asp Ile Ala Glu Val Leu Trp Asn Asp Phe Leu Lys His Asn Pro 35 40 45			144
acc gac cca acc tgg tat gat cgc gac cgc ttt att ctt tcc aac ggt Thr Asp Pro Thr Trp Tyr Asp Arg Asp Arg Phe Ile Leu Ser Asn Gly 50 55 60			192
cac gcg tcg atg ctg ctc tac agt ttg cta cat ctg acc ggt tac gac His Ala Ser Met Leu Leu Tyr Ser Leu Leu His Leu Thr Gly Tyr Asp 65 70 75 80			240
ctg ccg ctg gaa gaa ctg aag aac ttc cgt cag ttg cat tcg aaa acc Leu Pro Leu Glu Glu Leu Lys Asn Phe Arg Gln Leu His Ser Lys Thr 85 90 95			288
cca ggc cac ccg gag att ggc tat acg cca ggc gtt gaa acc acc acc Pro Gly His Pro Glu Ile Gly Tyr Thr Pro Gly Val Glu Thr Thr Thr 100 105 110			336
ggc ccg ctt gga caa ggt ttg gcg aac gcc gtc ggg ctg gcg ata gca Gly Pro Leu Gly Gln Gly Leu Ala Asn Ala Val Gly Leu Ala Ile Ala 115 120 125			384
gag cgt aca ctg gcg gcg cag ttt aac cag cca gac cat gag atc gtc Glu Arg Thr Leu Ala Ala Gln Phe Asn Gln Pro Asp His Glu Ile Val 130 135 140			432
gat cac ttc acc tat gtg ttt atg ggc gac ggc tgc ctg atg gaa ggt Asp His Phe Thr Tyr Val Phe Met Gly Asp Gly Cys Leu Met Glu Gly 145 150 155 160			480
att tcc cac gaa gtc tgt tcg ctg gca ggc acg ctg gga ctg ggc aag Ile Ser His Glu Val Cys Ser Leu Ala Gly Thr Leu Gly Leu Gly Lys 165 170 175			528
ctg att ggt ttt tac gat cac aac ggt att tcc atc gac ggt gaa aca Leu Ile Gly Phe Tyr Asp His Asn Gly Ile Ser Ile Asp Gly Glu Thr 180 185 190			576
gaa ggc tgg ttt acc gac gat acg gca aaa cgt ttt gaa gcc tat cac Glu Gly Trp Phe Thr Asp Asp Thr Ala Lys Arg Phe Glu Ala Tyr His 195 200 205			624
tgg cat gtg atc cat gaa atc gac ggt cac gat ccg cag gcg gtg aag Trp His Val Ile His Glu Ile Asp Gly His Asp Pro Gln Ala Val Lys 210 215 220			672
gaa gcg atc ctt gaa gcg caa agc gtg aaa gat aag ccg tcg ctg att Glu Ala Ile Leu Glu Ala Gln Ser Val Lys Asp Lys Pro Ser Leu Ile 225 230 235 240			720
atc tgc cgt acg gtg att ggc ttt ggt tcg ccg aat aaa gca ggt aag Ile Cys Arg Thr Val Ile Gly Phe Gly Ser Pro Asn Lys Ala Gly Lys 245 250 255			768

gaa gag gcg cac ggc gca cca ctg ggg gaa gaa gaa gtg gcg ctg gca Glu Glu Ala His Gly Ala Pro Leu Gly Glu Glu Glu Val Ala Leu Ala 260 265 270	816
cgg caa aaa ctg ggc tgg cac cat ccg cca ttt gag atc cct aaa gag Arg Gln Lys Leu Gly Trp His His Pro Pro Phe Glu Ile Pro Lys Glu 275 280 285	864
att tat cac gcc tgg gat gcc cgt gaa aaa ggc gaa aaa gcg cag cag Ile Tyr His Ala Trp Asp Ala Arg Glu Lys Gly Glu Lys Ala Gln Gln 290 295 300	912
agc tgg aat gag aag ttt gcc gcc tat aaa aag gct cat ccg caa ctg Ser Trp Asn Glu Lys Phe Ala Ala Tyr Lys Lys Ala His Pro Gln Leu 305 310 315 320	960
gca gaa gag ttt acc cga cgg atg agc ggt ggt tta ccg aag gac tgg Ala Glu Glu Phe Thr Arg Arg Met Ser Gly Gly Leu Pro Lys Asp Trp 325 330 335	1008
gag aaa acg act cag aaa tat atc aat gag tta cag gca aat ccg gcg Glu Lys Thr Thr Gln Lys Tyr Ile Asn Glu Leu Gln Ala Asn Pro Ala 340 345 350	1056
aaa atc gct acc cgt aag gct tcg caa aat acg ctt aac gct tac ggg Lys Ile Ala Thr Arg Lys Ala Ser Gln Asn Thr Leu Asn Ala Tyr Gly 355 360 365	1104
ccg atg ctg cct gag ttg ctc ggc ggt tcg gcg gat ctg gct ccc agc Pro Met Leu Pro Glu Leu Leu Gly Gly Ser Ala Asp Leu Ala Pro Ser 370 375 380	1152
aac ctg acc atc tgg aaa ggt tct gtt tcg ctg aag gaa gat cca gcg Asn Leu Thr Ile Trp Lys Gly Ser Val Ser Leu Lys Glu Asp Pro Ala 385 390 395 400	1200
ggc aac tac att cac tac ggg gtg cgt gaa ttt ggc atg acc gct atc Gly Asn Tyr Ile His Tyr Gly Val Arg Glu Phe Gly Met Thr Ala Ile 405 410 415	1248
gcc aac ggc atc gcg cac cac ggc ggc ttt gtg ccg tat acc gcg acg Ala Asn Gly Ile Ala His His Gly Gly Phe Val Pro Tyr Thr Ala Thr 420 425 430	1296
ttc ctg atg ttt gtt gaa tac gcc cgt aac gcc gcg cgg atg gcg gca Phe Leu Met Phe Val Glu Tyr Ala Arg Asn Ala Ala Arg Met Ala Ala 435 440 445	1344
ctg atg aaa gcg cgg cag att atg gtt tat acc cac gac tca att ggc Leu Met Lys Ala Arg Gln Ile Met Val Tyr Thr His Asp Ser Ile Gly 450 455 460	1392
ctg ggc gaa gat ggt ccg acg cac cag gct gtt gag caa ctg gcc agc Leu Gly Glu Asp Gly Pro Thr His Gln Ala Val Glu Gln Leu Ala Ser 465 470 475 480	1440

ctg cgc tta acg cca aat ttc agc acc tgg cga ccg tgc gat cag gtg	1488
Leu Arg Leu Thr Pro Asn Phe Ser Thr Trp Arg Pro Cys Asp Gln Val	
485 490 495	
gaa gcg gcg gtg ggc tgg aag ctg gcg gtt gag cgc cac aac gga ccg	1536
Glu Ala Ala Val Gly Trp Lys Leu Ala Val Glu Arg His Asn Gly Pro	
500 505 510	
acg gca ctg atc ctc tca agg cag aat ctg gcc cag gtg gaa cgt acg	1584
Thr Ala Leu Ile Leu Ser Arg Gln Asn Leu Ala Gln Val Glu Arg Thr	
515 520 525	
ccg gat cag gtt aaa gag att gct cgt ggc ggt tat gtg ctg aaa gac	1632
Pro Asp Gln Val Lys Glu Ile Ala Arg Gly Gly Tyr Val Leu Lys Asp	
530 535 540	
agc ggc ggt aag cca gat att att ctg att gcc acc ggt tca gag atg	1680
Ser Gly Gly Lys Pro Asp Ile Ile Leu Ile Ala Thr Gly Ser Glu Met	
545 550 555 560	
gaa att acc ctg caa gcg gca gag aaa tta gca gga gaa ggt cgc aat	1728
Glu Ile Thr Leu Gln Ala Ala Glu Lys Leu Ala Gly Glu Gly Arg Asn	
565 570 575	
gta cgc gta gtt tcc ctg ccc tcg acc gat att ttc gac gcc cag gat	1776
Val Arg Val Val Ser Leu Pro Ser Thr Asp Ile Phe Asp Ala Gln Asp	
580 585 590	
gag gaa tat cgg gag tcg gtg ttg cct tct aac gtt gcg gct cgc gtg	1824
Glu Glu Tyr Arg Glu Ser Val Leu Pro Ser Asn Val Ala Ala Arg Val	
595 600 605	
gcg gtg gaa gca ggt att gcc gat tac tgg tac aag tat gtt ggt ctg	1872
Ala Val Glu Ala Gly Ile Ala Asp Tyr Trp Tyr Lys Tyr Val Gly Leu	
610 615 620	
aaa ggg gca att gtc ggg atg acg ggt tac ggg gaa tct gct ccg gcg	1920
Lys Gly Ala Ile Val Gly Met Thr Gly Tyr Gly Glu Ser Ala Pro Ala	
625 630 635 640	
gat aag ctg ttc ccg ttc ttt ggc ttt acc gcc gag aat att gtg gca	1968
Asp Lys Leu Phe Pro Phe Phe Gly Phe Thr Ala Glu Asn Ile Val Ala	
645 650 655	
aaa gcg cat aag gtg ctg gga gtg aaa ggt gcc tga	2004
Lys Ala His Lys Val Leu Gly Val Lys Gly Ala	
660 665	

&lt;210&gt; 12

&lt;211&gt; 667

&lt;212&gt; PRT

&lt;213&gt; Escherichia coli

&lt;400&gt; 12

Met Ser Arg Lys Asp Leu Ala Asn Ala Ile Arg Ala Leu Ser Met Asp

6550-000086/POA

225                      230                      235                      240  
 Ile Cys Arg Thr Val Ile Gly Phe Gly Ser Pro Asn Lys Ala Gly Lys  
                                  245                      250                      255  
 Glu Glu Ala His Gly Ala Pro Leu Gly Glu Glu Glu Val Ala Leu Ala  
                                  260                      265                      270  
 Arg Gln Lys Leu Gly Trp His His Pro Pro Phe Glu Ile Pro Lys Glu  
                                  275                      280                      285  
 Ile Tyr His Ala Trp Asp Ala Arg Glu Lys Gly Glu Lys Ala Gln Gln  
                                  290                      295                      300  
 Ser Trp Asn Glu Lys Phe Ala Ala Tyr Lys Lys Ala His Pro Gln Leu  
 305                                   310                      315                      320  
 Ala Glu Glu Phe Thr Arg Arg Met Ser Gly Gly Leu Pro Lys Asp Trp  
                                  325                      330                      335  
 Glu Lys Thr Thr Gln Lys Tyr Ile Asn Glu Leu Gln Ala Asn Pro Ala  
                                  340                      345                      350  
 Lys Ile Ala Thr Arg Lys Ala Ser Gln Asn Thr Leu Asn Ala Tyr Gly  
                                  355                      360                      365  
 Pro Met Leu Pro Glu Leu Leu Gly Gly Ser Ala Asp Leu Ala Pro Ser  
                                  370                      375                      380  
 Asn Leu Thr Ile Trp Lys Gly Ser Val Ser Leu Lys Glu Asp Pro Ala  
 385                                   390                      395                      400  
 Gly Asn Tyr Ile His Tyr Gly Val Arg Glu Phe Gly Met Thr Ala Ile  
                                  405                      410                      415  
 Ala Asn Gly Ile Ala His His Gly Gly Phe Val Pro Tyr Thr Ala Thr  
                                  420                      425                      430  
 Phe Leu Met Phe Val Glu Tyr Ala Arg Asn Ala Ala Arg Met Ala Ala  
                                  435                      440                      445  
 Leu Met Lys Ala Arg Gln Ile Met Val Tyr Thr His Asp Ser Ile Gly  
                                  450                      455                      460



Leu Gly Glu Asp Gly Pro Thr His Gln Ala Val Glu Gln Leu Ala Ser  
 465 470 475 480  
 Leu Arg Leu Thr Pro Asn Phe Ser Thr Trp Arg Pro Cys Asp Gln Val  
 485 490 495  
 Glu Ala Ala Val Gly Trp Lys Leu Ala Val Glu Arg His Asn Gly Pro  
 500 505 510  
 Thr Ala Leu Ile Leu Ser Arg Gln Asn Leu Ala Gln Val Glu Arg Thr  
 515 520 525  
 Pro Asp Gln Val Lys Glu Ile Ala Arg Gly Gly Tyr Val Leu Lys Asp  
 530 535 540  
 Ser Gly Gly Lys Pro Asp Ile Ile Leu Ile Ala Thr Gly Ser Glu Met  
 545 550 555 560  
 Glu Ile Thr Leu Gln Ala Ala Glu Lys Leu Ala Gly Glu Gly Arg Asn  
 565 570 575  
 Val Arg Val Val Ser Leu Pro Ser Thr Asp Ile Phe Asp Ala Gln Asp  
 580 585 590  
 Glu Glu Tyr Arg Glu Ser Val Leu Pro Ser Asn Val Ala Ala Arg Val  
 595 600 605  
 Ala Val Glu Ala Gly Ile Ala Asp Tyr Trp Tyr Lys Tyr Val Gly Leu  
 610 615 620  
 Lys Gly Ala Ile Val Gly Met Thr Gly Tyr Gly Glu Ser Ala Pro Ala  
 625 630 635 640  
 Asp Lys Leu Phe Pro Phe Phe Gly Phe Thr Ala Glu Asn Ile Val Ala  
 645 650 655  
 Lys Ala His Lys Val Leu Gly Val Lys Gly Ala  
 660 665

<210> 13  
 <211> 27  
 <212> DNA

<213> Artificial

<220>

<223> Primer JWF 430

<400> 13

gctctagatg cagtggcaaa ctaaact

27

<210> 14

<211> 29

<212> DNA

<213> Artificial

<220>

<223> Primer JWF 449

<400> 14

tagctctccg tcacgttact agatctcag

29

<210> 15

<211> 29

<212> DNA

<213> Artificial

<220>

<223> Primer JWF 484

<400> 15

gacggatcct ataaggagca tcgctcatg

29

<210> 16

<211> 30

<212> DNA

<213> Artificial

<220>

<223> Primer JWF 529

<400> 16

tagctctccg tcacgttact gacgtcgaag

30

<210> 17

<211> 20

<212> DNA

<213> Artificial

<220>

<223> Primer JWF 501

<400> 17

gacaggaata aggagcatcg

20

<210> 18  
<211> 20  
<212> DNA  
<213> Artificial

<220>  
<223> Primer JWF 499

<400> 18  
ggagggtaaac ggtacgtggt

20

<210> 19  
<211> 28  
<212> DNA  
<213> Artificial

<220>  
<223> Primer JWF 541

<400> 19  
ggaattcgca taaacaggat cgccatca

28

<210> 20  
<211> 26  
<212> DNA  
<213> Artificial

<220>  
<223> Primer JWF 542

<400> 20  
ctggatcctt aagccacgcg agccgt

26

<210> 21  
<211> 29  
<212> DNA  
<213> Artificial

<220>  
<223> Primer JWF 610

<400> 21  
gtggatcctt aatccgttca tagtgtaaa

29

<210> 22  
<211> 27  
<212> DNA  
<213> Artificial

<220>  
<223> Primer JWF 611

<400> 22  
tgggatccat gagaaagccg actgcaa 27

<210> 23  
<211> 20  
<212> DNA  
<213> Artificial

<220>  
<223> Primer JWF 625

<400> 23  
gttcgctcagt gcaggatgga 20

<210> 24  
<211> 22  
<212> DNA  
<213> Artificial

<220>  
<223> Primer JWF 626

<400> 24  
gttcaggcgt gagttttctg ct 22

<210> 25  
<211> 28  
<212> DNA  
<213> Artificial

<220>  
<223> Primer JWF 541

<400> 25  
ggaattcgca taaacaggat cgccatca 28

<210> 26  
<211> 26  
<212> DNA  
<213> Artificial

<220>  
<223> Primer JWF 542

<400> 26  
ctggatcctt aagccacgcg agccgt 26

<210> 27  
<211> 21  
<212> DNA  
<213> Artificial

&lt;220&gt;

&lt;223&gt; Primer JWF 636

&lt;400&gt; 27

tccgtactgc gcgtattgag a

21

&lt;210&gt; 28

&lt;211&gt; 20

&lt;212&gt; DNA

&lt;213&gt; Artificial

&lt;220&gt;

&lt;223&gt; Primer JWF 637

&lt;400&gt; 28

agaggcgagt ttttcgacca

20

&lt;210&gt; 29

&lt;211&gt; 20

&lt;212&gt; DNA

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